



SEQUENCE LISTING

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<120> PLANT NUCLEOTIDE SUGAR PYROPHOSPHATASE/PHOSPHODIESTERASE
(NPPASE), METHOD OF PRODUCTION, USE IN THE MANUFACTURE OF TESTING
DEVICES AND IN THE PRODUCTION OF TRANSGENIC PLANTS

<130> U015575-8

<140> 10/520696
<141> 2005-01-06

<150> PCT/ES03/000363
<151> 2003-07-15

<160> 24

<170> PatentIn version 3.3

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<213> HORDEUM VULGARE CV. SCARLETT

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<223> N-terminal end of soluble NPPase

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Ala Ala Val Arg Ala Ser Pro Asp Leu Leu Gly Ser Arg Gly Glu
1 5 10 15

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<223> Xaa can be Gln or Lys

<220>

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<223> Xaa can be Leu or Ile

<220>

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<222> (10)..(10)

<223> Xaa can be Lys or Gln

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Ala Ser Tyr Pro Gly Xaa Thr Ser Xaa Xaa Arg

1

5

10

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<223> Tryptic sequence of soluble NPPase

<220>

<221> MISC_FEATURE

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<400> 3

His Ala Pro Ala Asp Thr Val Thr Xaa Gly Arg

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5

10

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<223> Tryptic sequence of soluble NPPase

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Ala Pro Pro Tyr Pro

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5

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<223> Tryptic sequence of soluble NPPase

<400> 5

Ala Trp Val Thr Val Glu Phe Lys
1 5

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<222> (3)..(3)
<223> Xaa can be Ile or Leu

<220>
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<223> Xaa can be Ile or Leu

<400> 6

Xaa Ser Xaa Glu Gly Xaa Trp Arg
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<220>

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<223> N-terminal end of soluble NPPase

<400> 7

Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly Asp Gln
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<210> 8
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<213> ORYZA SATIVA

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 8

Phe Gln Leu Leu Asn Gln Arg Tyr Asp Phe Ser Phe Ala Leu Glu Thr
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Gly Gly Leu Glu Asn Pro Lys
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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 9

Leu Val Ala Val Ser Glu Ala Leu Ser Phe Lys
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Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met
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<210> 11

<211> 10

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<223> Tryptic sequence (MS/MS) of soluble NPPase

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Thr Ala Ala Gly Thr Leu Thr Phe Asn Arg
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<210> 12

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<220>

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Asp Pro Gly Phe Leu His Thr Ala Phe Leu Arg
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Ala Pro Asp Phe Pro Gly Gln Asn Ser Leu Gln Arg
1 5 10

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<211> 9
<212> PRT
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<220>
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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 14

Ile Ile Val Phe Gly Asp Met Gly Lys
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<210> 15
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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 15

Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys
1 5 10

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<400> 16

Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg
1 5 10

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<220>
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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 17

Val Tyr Asp Ser Phe Tyr Val Glu Arg
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<223> Primer of the 5' region of NPPase

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ggcgttgctc ggcgacca 18

<210> 19
<211> 19
<212> DNA
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<223> Primer of the 3' region of NPPase

<400> 19
gaggcgagcg tgggtggga 19

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<211> 2186
<212> DNA
<213> ORYZA SATIVA

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<223> complete cDNA of rice NPPase

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tcgctggaag ggttccagcc gctgtcgaag atcgccgtcc acaaggccac cgtcgacctc 180

cacggctccg cgttcgtcag cgccacgccg gcgttgctcg gcgaccaggg agaagacaca	240
gagtgggtca cggtgaaata cggtgggca aacccttccg ctgacgactg gattgctgtc	300
ttctctccgg ccgatttcat ctcggttct tgccctaate cttccagata cccggatgag	360
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<210> 21
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<213> ORYZA SATIVA

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<220>
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<223> Amino acid sequence of rice NPPase

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<400> 21

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Met Val Ser Arg Lys Arg Gly Gly Gly Gly Gly Val Ala Met Ala Val
1           5           10           15

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Ala Met Leu Leu Ala Ala Ala Ser Ala Ser Arg Pro Ser Ser Ser Leu
          20           25           30

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Glu Gly Phe Gln Pro Leu Ser Lys Ile Ala Val His Lys Ala Thr Val
35           40           45

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Asp Leu His Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly
50           55           60

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Asp Gln Gly Glu Asp Thr Glu Trp Val Thr Val Lys Tyr Gly Trp Ala
65           70           75           80

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Asn Pro Ser Ala Asp Asp Trp Ile Ala Val Phe Ser Pro Ala Asp Phe
          85           90           95

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Ile Ser Gly Ser Cys Pro Asn Pro Ser Arg Tyr Pro Asp Glu Pro Leu
100           105           110

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Leu Cys Thr Ala Pro Ile Lys Tyr Gln Phe Ala Asn Tyr Ser Ala Asn
115 120 125

Tyr Val Tyr Trp Gly Lys Gly Ser Ile Arg Phe Gln Leu Ile Asn Gln
130 135 140

Arg Tyr Asp Phe Ser Phe Ala Leu Phe Thr Gly Gly Leu Glu Asn Pro
145 150 155 160

Lys Leu Val Ala Val Ser Glu Ala Ile Ser Phe Lys Asn Pro Lys Ala
165 170 175

Pro Val Tyr Pro Arg Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met Thr
180 185 190

Val Thr Trp Thr Ser Gly Tyr Asp Ile Ser Glu Ala Tyr Pro Phe Val
195 200 205

Glu Trp Gly Met Val Val Ala Gly Ala Ala Ala Pro Thr Arg Thr Ala
210 215 220

Ala Gly Thr Leu Thr Phe Asn Arg Gly Ser Met Cys Gly Asp Pro Asp
225 230 235 240

Arg Thr Val Gly Trp Arg Asp Pro Gly Phe Ile His Thr Ala Phe Leu
245 250 255

Arg Asp Leu Trp Pro Asn Lys Glu Tyr Tyr Tyr Lys Ile Gly His Glu
260 265 270

Leu Ser Asp Gly Ser Ile Val Trp Gly Lys Gln Tyr Thr Phe Arg Ala
275 280 285

Pro Pro Phe Pro Gly Gln Asn Ser Leu Gln Arg Ile Ile Val Phe Gly
290 295 300

Asp Met Gly Lys Ala Glu Arg Asp Gly Ser Asn Glu Phe Ala Asn Tyr
305 310 315 320

Gln Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Val Glu Asp Leu Asp
325 330 335

Asn Tyr Asp Ile Val Phe His Ile Gly Asp Leu Pro Tyr Ala Asn Gly
340 345 350

Tyr Ile Ser Gln Trp Asp Gln Phe Thr Ala Gln Val Ala Pro Ile Thr
355 360 365

Ala Lys Lys Pro Tyr Met Ile Ala Ser Gly Asn His Glu Arg Asp Trp
370 375 380

Pro Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys
385 390 395 400

Gly Val Pro Ala Glu Thr Met Tyr Tyr Tyr Pro Ala Glu Asn Arg Ala
405 410 415

Asn Phe Trp Tyr Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Ile Ala
420 425 430

Asp Ser Glu His Asp Trp Arg Glu Gly Thr Asp Gln Tyr Lys Phe Ile
435 440 445

Glu Gln Cys Leu Ser Thr Val Asp Arg Lys His Gln Pro Trp Leu Ile
450 455 460

Phe Ala Ala His Arg Val Leu Gly Tyr Ser Ser Asn Trp Trp Tyr Ala
465 470 475 480

Asp Gln Gln Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Arg
485 490 495

Leu Trp Gln Arg His Arg Val Asp Val Ala Phe Phe Gly His Val His
500 505 510

Asn Tyr Glu Arg Thr Cys Pro Met Tyr Gln Ser Gln Cys Val Ser Gly
515 520 525

Glu Arg Arg Arg Tyr Ser Gly Thr Met Asn Gly Thr Ile Phe Val Val
530 535 540

Ala Gly Gly Gly Gly Ser His Leu Ser Asp Tyr Thr Ser Ala Ile Pro

545		550		555		560
Lys Trp Ser Val Phe Arg Asp Arg Asp Phe Gly Phe Val Lys Leu Thr						
	565			570		575
Ala Phe Asn His Ser Ser Leu Leu Phe Glu Tyr Lys Lys Ser Ser Asp						
	580			585		590
Gly Lys Val Tyr Asp Ser Phe Thr Val Glu Arg Asp Tyr Arg Asp Val						
	595			600		605
Leu Ser Cys Val His Asp Ser Cys Leu Pro Thr Thr Leu Ala Ser						
	610			615		620

<210> 22
 <211> 1268
 <212> DNA
 <213> HORDEUM VULGARE CV. SCARLETT

<220>
 <221> misc_feature
 <223> Incomplete cDNA of barley NPPase

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gcagaactcg ctgcagcgta tcatcgctctt cggtgacatg ggaaaggcgg agaggggacgg	120
atcaaacgag ttcgccaact accagccggg gtcgctcaac acgacggaca ggctgattga	180
agatctggac aactacgaca tcgtcttcca catcggcgac atgccctacg ccaacgggta	240
cctctcccag tgggaccagt tcaccgcaca ggtcgcccc atcagcgcca agaaacccta	300
catggttgca agcggcaacc acgagaggga ctggcccaac accggcgggt tcttcgacgt	360
caaggactcc ggcggcgaat gcggcggtgcc ggccgagacc atgtactact accccgccga	420
aaacagggca aacttctggt acaaggtgga ctacgggatg ttccggttct gcgtggggga	480
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gacggtggac cggaagcacc agccgtggct catcttcacg gcgcaccggg tgctgggcta	600
ctcctccaac tcgtggtacg ccgaccaggg ctcttcgag gagcccgagg gacgggagag	660
cctgcagaag ctgtggcagc gctaccgcgt cgacatcgcc tccttcggcc acgtccacaa	720

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ctacgagcgc acatgcccg cttaccagag ccagtgcgtc aacgccgaca agaccacta 780
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caagctcacc gcattcaacc actcctcgt tctcttcgag tacatgaaga gcagcgacgg 960
caaggtctac gactccttca ccatccacag ggattaccgc gacgtgtca gctgcgtgca 1020
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cagctgcaca atttatatgt gctagtaaaa agatcatgca agaggtgggt gtatgctcgt 1200
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<213> HORDEUM VULGARE CV. SCARLETT

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<220>
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<223> Amino acid sequence deduced from the cDNA of barley NPPase

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<400> 23

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Ser Asp Gly Ser Val Val Trp Ala Lys Pro Tyr Thr Phe Arg Ala Pro
1          5          10          15

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```

Pro Thr Pro Gly Gln Asn Ser Leu Gln Arg Ile Ile Val Phe Gly Asp
20          25          30

```

```

Met Gly Lys Ala Glu Arg Asp Gly Ser Asn Glu Phe Ala Asn Tyr Gln
35          40          45

```

```

Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Ile Glu Asp Leu Asp Asn
50          55          60

```

```

Tyr Asp Ile Val Phe His Ile Gly Asp Met Pro Tyr Ala Asn Gly Tyr
65          70          75          80

```

```

Leu Ser Gln Trp Asp Gln Phe Thr Ala Gln Val Ala Pro Ile Ser Ala

```

85

90

95

Lys Lys Pro Tyr Met Val Ala Ser Gly Asn His Glu Arg Asp Trp Pro
 100 105 110

Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys Gly
 115 120 125

Val Pro Ala Glu Thr Met Tyr Tyr Tyr Pro Ala Glu Asn Arg Ala Asn
 130 135 140

Phe Trp Tyr Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Val Gly Asp
 145 150 155 160

Ser Glu His Asp Trp Arg Glu Gly Thr Pro Gln Tyr Lys Phe Ile Glu
 165 170 175

Glu Cys Leu Ser Thr Val Asp Arg Lys His Gln Pro Trp Leu Ile Phe
 180 185 190

Thr Ala His Arg Val Leu Gly Tyr Ser Ser Asn Ser Trp Tyr Ala Asp
 195 200 205

Gln Gly Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Lys Leu
 210 215 220

Trp Gln Arg Tyr Arg Val Asp Ile Ala Ser Phe Gly His Val His Asn
 225 230 235 240

Tyr Glu Arg Thr Cys Pro Leu Tyr Gln Ser Gln Cys Val Asn Ala Asp
 245 250 255

Lys Thr His Tyr Ser Gly Thr Met Asn Gly Thr Ile Phe Val Val Ala
 260 265 270

Gly Gly Gly Gly Ser His Leu Ser Ser Tyr Thr Thr Ala Ile Pro Lys
 275 280 285

Trp Ser Ile Phe Arg Asp His Asp Tyr Gly Phe Thr Lys Leu Thr Ala
 290 295 300

Phe Asn His Ser Ser Leu Leu Phe Glu Tyr Met Lys Ser Ser Asp Gly
305 310 315 320

Lys Val Tyr Asp Ser Phe Thr Ile His Arg Asp Tyr Arg Asp Val Leu
325 330 335

Ser Cys Val His Asp Ser Cys Phe Pro Thr Thr Leu Ala Ser
340 345 350

<210> 24
<211> 39
<212> DNA
<213> HORDEUM VULGARE CV. SCARLETT

<220>
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<223> Primer of the 5' region of NPPase

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39